

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 26, 2001, 09:16:10 ; Search time 2192.46 Seconds

(without alignments)

23115.284 Million cell updates/sec

Title: US-08-482-402A-2

Perfect score: 3072

Sequence: 1 gagggcaatttggggcccat.....atactgcaaaaaaaaaaa 3072

Scoring table: IDENTITY_NUC

Gap0 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 10%

Listing first 45 summaries

Database : GenBank

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_lov:*

6: gb_pat:*

7: gb_ph:*

8: gb_p1:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_v1:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_om:*

20: em_or:*

21: em_lov:*

22: em_pat:*

23: em_ph:*

24: em_pl:*

25: em_ro:*

26: em_sts:*

27: em_sy:*

28: em_un:*

29: em_v1:*

30: em_htgo_hum:*

31: em_htgo_inv:*

32: em_htgo_rod:*

33: em_htg_hum:*

34: em_htg_inv:*

35: em_htg_rod:*

36: em_htg_other:*

	Result No.	Score	Match Length	DB ID	Description
	1	99.6	3060	9	HUMTPOC
	2	3004	97.8	3048	6 AR092419 Sequence
	3	3004	97.8	3048	9 HUMTPOA
	4	2991.4	97.4	3027	9 HSTPO
	5	2803	91.2	2847	6 A92132 Sequence 1
	6	2652	86.3	2877	9 HUMTPOB
	7	2649.6	86.2	2845	9 HSASTPO2
	8	2511.4	81.8	2546	6 E23825 Antigen for
	9	1655.2	53.9	3237	10 RNTPO
	10	1628.6	53.0	3291	10 MMTPER
	11	1441.8	46.9	2777	10 RATTPOFR
	12	970	31.6	1046	9 HUMTPOD
	13	516	16.8	1996	9 HUMTP007
	14	516	16.8	160674	2 AC060811 Homo sapi
	15	510.4	16.6	1142	4 SSTPORI
	16	469.8	15.3	2238	9 S56200 myeloperoxi
	17	469.8	15.3	2261	6 A08802 H.sapiens g
	18	469.8	15.3	2568	9 HUMMYP
	19	469.8	15.3	3213	9 HSMPOR
	20	469.8	15.3	3215	6 E12629 DNA encodi
	21	469.8	15.3	3215	9 HUMMPO
	22	461.4	15.0	2666	10 MUSEPO
	23	461.4	15.0	2694	10 MUSEPP
	24	445	14.5	2740	10 MMMPO
	25	438.2	14.3	2558	9 HSEP
	26	433.6	14.1	2915	3 AB022196 Clona int
	27	427.8	13.9	3846	5 AF349034 Homo sapi
	28	417	13.6	5510	9 D86983 Human mRNA
	29	417	13.6	6847	9 AF200348 Homo sapi
	30	411.8	13.4	2814	5 AF378824 Danio rer
	31	397.4	12.9	2768	9 HSU39573 Human salivary
	32	397	12.9	3179	3 AB022197 Halocyphus
	33	395.2	12.9	3449	3 AB028841 Branchios
	34	386	12.6	2710	4 BOVLPO
	35	379.6	12.4	2780	4 AF027970 ovis aries
	36	368.8	12.0	2634	4 CDR131675 Camelus d
	c	37	344.8	11.2	172445 9 AC009471 Homo sapi
		38	338.4	11.0	4359 9 S46243 thyroid per
	c	39	317	10.3	300829 3 AE003475 Drosophil
	c	40	305	9.9	80254 2 AC019531 Drosophil
	c	41	301.8	9.8	5 XU068724 Xenopus lae
	c	42	295	9.6	4871 3 DMU11052 Drosophila
	c	43	289.4	9.4	1399 9 HUMLPO
	c	44	265	8.6	1328 9 HUMTP008
	c	45	261.2	8.5	1448 5 AF364820 Xenopus 1

ALIGNMENTS

RESULT	1
HUMTPOC	3060 bp mRNA
LOCUS	Homo sapiens thyroid peroxidase (TPO) mRNA, complete cds.
DEFINITION	
ACCESSION	M17755
VERSION	M17755.2
KEYWORDS	GI:4680720
SOURCE	human.
ORGANISM	Homo sapiens
	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo.
REFERENCE	1 (bases 732 to 1573)
AUTHORS	Seto, P., Hirayu, H., Magnusson, R.P., Gestautas, J., Portmann, L., Decroot, L.J. and Rapoport, B.
TITLE	Isolation of a complementary DNA clone for thyroid microsomal antigen. Homology with the gene for thyroid peroxidase
JOURNAL	J. Clin. Invest. 80 (4), 1205-1208 (1987)
MEDLINE	8808367
REFERENCE	2 (bases 1 to 3060)
AUTHORS	Magnusson, R.P., Chazenbalk, G.D., Gestautas, J., Seto, P., Filetti, S.,

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

DOB	1141	CA CG GG CG CC TT CG GG ACT CG GG CG CC TT CG GG ACT CG GG CG CC TT CG GG AC CG GG CCT	1200
QDY	1201	gg gg cc tt gt gc cc gg ag gg cc gg gg aa ac cc cc gg gg ag gg ac cc gg gg cc tt ct cc tg gg	1260
DOB	1201	GG GG CT GT AG CG CC GG AA CC CG GG AG AG AC CC CG GG CCT TG CT GT CG CC TT GT GG CC	1260
QDY	1261	gg ag gg cc gg cc gg ag gg gg cc tt ct gt gg gg cc tt ct gt gg gg cc tt ct gt gg gg	1320
DOB	1261	GG AG AG GG CC GG CC AG GG AG GG TCC CT CG CC AG CG AC CG AC CG CC TT GT GG CT GT GG CC	1320
QDY	1321	gag caca ac cc gg cc tt gt gg cc gg gg cc tt ct ca ag gg cc tt ca aat tg cc aact gg gg cc	1380
DOB	1321	GAG CACA AC CC GG CC TT GT GG CC GG GT CA AG GG CC TT CA AT CG CA TG GG CC GT AG TG GG CC	1380
QDY	1381	gt gt ac cc ag gg ag gg cc gg cc gg gg cc tt ct gt cc ag gg ac cc tt aat cc ct gg gg tt	1440
DOB	1381	GT GT AC CC AG GG CG CC GG CG CA AG GT CG CC TT GG GG CT GT CG CC AG AT CG AT CA CC CG AT	1440
QDY	1441	tac at cc cagg at ct tt gg ac cc gg cc gg gg cc tt ct cc ag gg ac cc tt cc tg gg gg cc tt	1500
DOB	1441	TAC AT CC CAG G AT CT TT GG AC CC GG CC TT CC AG CAG T AC GT GG GT CC TT AT GA AG CC	1500
QDY	1501	tat gact cc ac cc gg cc aa cc cc ac ct gt gtc ca ac ct gt tt ct cc ac cc gg cc tt cc gg ct tc	1560
DOB	1501	TAT GACT CC AC CC GG CA AA CC CC AC CT GT GTC CA AC CT GT TT CT CC AC GG CC TT CC GG CT TC	1560
QDY	1561	gg cc at gg cc ag gg cc at gg cc tt cc ac cc gg cc tt cc ac cc gg cc tt cc ac cc gg cc tt	1620
DOB	1561	GG CC AT GG CC AC AG AT CC AC CC GG CT GT GG AG GG CT GT GG AG GG CC AT CC AG CC CC	1620
QDY	1621	gac ct gg cc gg ct gt gg ct gg ac cc gg cc tt ct cc ac cc gg cc tt cc ac cc gg cc tt	1680
DOB	1621	GAC CT GG CC AC AG AT CC AC CC GG CT GT GG AG GG CT GT GG AG GG CC AT CC AG CC CC	1680
QDY	1681	99 gt gg tt gg cc ac cc tt ac cc gg gg cc tt ct gt gg ca ag cc gg cc aa ct cc gg cc tt	1740
DOB	1681	99 GT GG TT GG CC AC CC TA AT CG AG GG CC TT CT GT GG AG GG CC AT CC AG CC CC	1740
QDY	1741	gat ca ct gt gta a ac gg gg ct tt gt gg cc tt cc ac cc gg cc tt cc ac cc gg cc tt	1800
DOB	1741	GAT CA CT GT GAT GAA AG GG AG GT CG GG AA AG GG CT TT GT GG AG GG CC AT CC AG CC CC	1800
QDY	1801	tt gg at ct gg cc tt ca ac ct gt gg cc tt cc ac cc gg cc tt cc ac cc gg cc tt cc ac cc gg	1860
DOB	1801	TT GG AC TA CT GG GT CC TA CA CT GT GAA GAG GG CC GG GAC AC GG GT CC AT AA GT	1860
QDY	1861	gat gt gg ag gg gt ct tag ct gta a aa ac tt ct cc cagg gg ct gg ac cc gg cc tt	1920
DOB	1861	GAT GT GG AG GT CT GG AC CC TT GT GG AG AC CC GG CT GG AC CC TT GT GG AG AC CC GG CT	1920
QDY	1921	at cc gg cc ag gg cc tt cc ac cc gg cc tt cc ac cc gg cc tt cc ac cc gg cc tt	1980
DOB	1921	AT CG CA CG AG CG AG GT GG CC AC AA GA AT CT GT GG ACT GT FA CA NG AT CT GT GA CA AC ANC	1980
QDY	1981	gat gt ct gg gg ag gg ct tag ct gta a aa ac tt ct cc cagg gg ct gg ac cc gg cc tt	2040
DOB	1981	GAT GT GG AG GT CT GG AC CC TT GT GG AG AC CC GG CT GG AC CC TT GT GG AG AC CC GG CT	2040
QDY	2041	tt tg cc tt ct ct at gg gg ag gg ct tag ct gta a aa ac tt ct cc cagg gg ct gg ac cc gg cc tt	2100
DOB	2041	TT TG CC TT CT CT AT GG GG AG GG CT GG AC CC TT GT GG AG AC CC GG CT GG AC CC TT GT GG	2100
QDY	2101	gaga ac cc ag cc gt ct cc ac gg cc tt cc ac cc gg cc tt cc ac cc gg cc tt cc ac cc gg	2160
DOB	2101	GAG A AG CC AG CG AG GT CT GG AG CC AT CC AG GG GT CG AG CC AT CC GT GG AG AC CC TT GT GG	2160
QDY	2161	cgg gt cat ct gt gt gg ac ac cc ac tt cc ac cc gg cc tt cc ac cc gg cc tt cc ac cc gg cc	2220
DOB	2161	CG GG GT CAT CT GT GT GG AG CC AT CC AG GG GT CG AG CC AT CC GT GG AG AC CC TT GT GG	2220
QDY	2221	aa at cc cc gg ag gg act tt gg ct tt gt gg ac cc tt ac tt cc ac cc gg cc tt cc ac cc gg	2280
DOB	2221	AA AT TT CC CG AG AG AT TT GT GG AG CC AT CC AG GG GT CG AG CC AT CC GT GG AG AC CC TT GT GG	2280

RESULT	2	BASE COUNT
AR092419	G	ORIGIN
LCUCS		
DEFINITION		
VERSION		
KEYWORDS		
SOURCE		
ORGANISM		
REFERENCE		
AUTHORS		
TITLE		
JOURNAL		
FEATURES		
Source		

RESULT 2
AR09219
AR09215
AR09216
AR09217
AR09218
AR09210
AR09211
AR09212
AR09213
AR09214

LOCUS AR09241g 3048 bp DNA
DEFINITION Sequence 2 from patent US 59998153.
ACCESSION ZP09241g

ACCUSATION AR092419.1 GI:100191
VERSION :
KEYWORDS :

SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1. (bases 1 to 3048) Unclassified.

AUTHORS Baker, J.R. Jr. and Koenig, R.J.
TITLE Thyroid peroxidase epitope region
TOURNAI Danton et al.
TYPE 5000153-2, 07-DEC-1990

JOURNAL FEATURES SOURCE Patent: US 3,320,113 A 2/23/1967, loc. 3048
Location/Qualifiers 1

Journal	2.1.1995	/organism="unknown"	566
BASE COUNT	671	a	881
ORIGIN	930	c	g

RUDPHRGASINTALARWLPVYEDFSQPQWNPFLYFLNQFPLPPVREVRHIVSNE
VYTDQDRSYDLIMAWGOTDHDAFTPOSTISKAFFGGGADCQMCCTCENOPCPFQIOLPE
EARPAAGTACCLPQYRSSAAGTQGDQGLAGNLNTRNQPMQGTLTSFLDAVSTVQGSSP
AUERLERNWNTSAEGLLRLYHARLDRSGRAYLTFPVPRPACAPSPGIPBTRGPQFPLA
GDCRASEVPSLTAHTLWLRHNRNLAAKALKAIAHNSADAVYQEARVKVGAHLQHITI
DHDYTRPLGAEPAQYQVYEGDSTAFNQFSTAFNQFSTAFNQFSTAFNQFSTAFNQFSTAFNQF
QEPBDPLPQWLNQFSPWLNQFSPWLNQFSPWLNQFSPWLNQFSPWLNQFSPWLNQFSP
DLYKHPDNIDWUJGLAENLPLPARTGPFLFACLIGKQMLARLDGDFWENWNSHYFTDA
ORRELEKHSLSRVTCDNTGLTRYPMDAFQVGRGKPFEDFECRCDSTPGMNLAEWRFETPOD
DKCGCPESVHFWYFQHCEESGRVYUWYSCRHGFYELQGRQJLCTQEGWDFPQCLKD
NECADGHPICRASARCTNKGQFQCLADCPYELQGKSTLPISETGGTPELJRCGKHQAQVTSQRAAQD
ALLIGGPAQTLSTVYICRWTGKTKSTLPISETGGTPELJRCGKHQAQVTSQRAAQD
SEDEGASSEGRDTHRLPRAA."

Y	2240	agtcttgtacagcatactcggatataaccctggaggaaaccttccccaag	2299	COMMENT	OS	Unidentified
Y	2050	AGTCCTGTACAGCATACTCGATTAACCTGGAGGCCCTGGAACTTCCCAAG	2109		PN	JP 199094833-A/1
Y	2300	acgacaagtgtggctcccgagagggtggagaattggactttggactgtggagggt	2359		PD	09-BPR-1999
Y	2110	ACGACAACTGTGGCTTCCACAGAGCGTGGAAATGGACTTGTGCACTGTGAGGAGT	2169		PF	19-SEP-1997 JP 1997273743
Y	2360	ctggggggcgcggtgttattctggccggatgggtatggctcaaggccggggac	2419		PR	MASAO FUKUSHIMA
Y	2170	CTGGGAACGGCGTGTGGTATTCTGGCCACGGGTATGAGCTTCAAGCCGGAGC	2229		PC	G01N33/53,C12N9/08,C12N15/09,G01N33/531,G01N33/564//(C12N9/08,
Y	2420	agtcacttgtacccaggaaaggatggattccaggctccctctggcaaaatgtggaaacg	2479		PC	C12N15/91,
Y	2230	AGTCATCTGACCCAGGAACGATGGATTCACGGCTCCCTCTGAAAGATGTGACG	2289		PC	C12N15/00,
Y	2480	agtgtggcaggagggtggccaccctccctggccaggctctggagggtggaaaccaaaag	2539		CC	Strandedness: Double;
Y	2290	AGTCAGACGGTGCACGCCACCCCCCTGCCACGGCTCTGCAAGGGTACGGTAC	2349		CC	Topology: Linear;
Y	2540	ggggctccagggtgtctggccggaccctcaaggatggaggatggggaaactctgg	2599		PH	Location/Qualifiers
Y	2350	GGGGCTTCCACGTGTCTGGGGACCCCTAGAGTTAGGACGATGGAGAACCTGGC	2409		FT	Key
Y	2600	tagactccggagggtccctgggtgacttggatctccatgtcgctggctgtctgtga	2659		FT	source
Y	2410	TAGACCTGGAGGCCCTGGTCACTTGATCCTCACCTGGTAC	2469		FT	/organism="Unidentified".
Y	2660	tgggggtcttggagggtcttggagggtcttggagggtcttggagggtcttggagggt	2719		FT	Location/Qualifiers
Y	2470	TGGGGGCTTCGAGGCTCACCTGAGGGTATTCAGGGTACGGCATGGACTA	2529		FT	1. 2546
Y	2720	aatccaaactcccaactctcgagaaactcccgaggatcggtggaaactcggtgg	2779		FT	1. 'Unidentified'.
Y	2530	ATTCACACTTCCACATCTCGAGAACGGGAACTCCGAGCTGGAGATGGAAAGC	2589		FT	1. 2546
Y	2780	accaggccgttggggacttcaccggcacttcggaggacttcggaggatggggatgt	2839		FT	/organism="Unidentified".
Y	2590	ACCACCCGCTGGGGACCTCACCGACGGCCACCTCAGACTCGAGGGAGTG	2649		FT	/organism="Unidentified".
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Y	2710	GGACAGTGGAGAACACTTCATGTCACCAAAATCACGGTAGACTTTCAAAACAG	2769		FT	/organism="Unidentified".
Y	2960	gcaaatcgggaaatcaggaggactttttcccaacacgggttaatcttagatgttc	3019		FT	/organism="Unidentified".
Y	2770	GCAATGGAAATCACGGAGCACTGTTTCCCCAACACGGTTAAATCTAGTACATGTC	2829		FT	/organism="Unidentified".
Y	3020	gtatgttacttcggc	3035		FT	/organism="Unidentified".
Y	2830	GTAGTTACTTCAGGC	2845		FT	/organism="Unidentified".
Y	8			RESULT	OS	Unidentified
Y	23825			LOCUS	E23825	2546 bp
Y				DEFINITION		DNA
Y				ACCESSION		Antigen for immunoassaying antihuman thyroid peroxidase antibody
Y				KEYWORDS		and recombinant human thyroid peroxidase.
Y				REFERENCE	E23825	E23825
Y				REFERENCE	JP 199094833-A/1.	GI:13024570
Y				ORGANISM		unidentified.
Y				REFERENCE		unclassified.
Y				AUTORS	1 (bases 1 to 2546)	Masso, F.
Y				TITLE		Antigen for immunoassaying antihuman thyroid peroxidase antibody

Qy	1013	cggccaaccggaggcaggatgaacgggttgcacctgtttcgtggactgtggcgttccacgggt 1072			
Db	790	CGGCCAACCCGGCGAGAGATGAACGGTTGACCTGGTCCACCGTGT 849			
Qy	1073	atggcaactccccccttagaggaggactggggaaactggaccatgtggaaactggggactgtgc 1132			
Db	850	ATGGCACTCCCGGGCTAGAGGCAAGTGGCAACTGGGGTACCTGGTCCACCGTGT 909			
Qy	1133	tccgcgtccacgcgcgtccggactccggcggactccggcggacttgcgtccgtggccac 1192			
Db	910	TCCGGCAGTCACGGGCTCCGGGACTCGGGGGACTGGGGACTCCGGCTGTGGCAAGGGCTGC 969			
Qy	1193	ggcgctcgccgtgtggccggactggggggcaaccggaggggggggggggggggggggggggg 1252			
Db	970	GGGCGCTGGGGCTGTGGGGGGATCAGGGGGATGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1029			
Qy	1253	tccggccggaggacgg 1312			
Db	1030	TCCGGGGAGACGG 1089			
Qy	1313	ggctgcggcggaggaccaaccggccgtgggggggggggggggggggggggggggggggggg 1372			
Db	1090	GGTGGCGGAGGAGGG 1149			
Qy	1373	cgggcgggtgttacggaggaggcggcgagggtgggggggggggggggggggggggggggg 1424			
Db	1150	CGGACGGCGTGTACCAAGGGGCCGCAAGGTCGTTGGGGCTCTGACACAGGT 1201			
RESULT 14					
LOCUS	AC060811	160674 bp	DNA	HTG	04-MAY-2001
DEFINITION	Homo sapiens	chromosome 2	clone	RP11-112B11	map 2, WORKING DRAFT
ACCESSION	AC060811	SEQUENCE, 15	unordered pieces.		
VERSION	AC060811.3	GI:1783741			
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT.				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1	(bases 1 to 160674)			
AUTHORS	Birren, B., Linton, L., Nusbaum, C., and Lander, E.				
TITLE	Homo sapiens chromosome 2, clone RP11-112B11				
JOURNAL	Unpublished				
REFERENCE	2	(bases 1 to 160674)			
AUTHORS	Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, M., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguski, M., Boukhalter, B., Brown, A., Burkett, G., Campopiano, A., Castile, A., Choepel, Y., Colangelo, M., Collins, S., Collimore, A., Cooke, P., Dearellano, K., Dewart, K., Diaz, J. S., Dodge, S., Domingo, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardon, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Haggas, B., Heaford, A., Horton, L., Howland, J. C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, P., Klein, J., Larocque, K., Lanzares, R., Landers, T., Lehnhofer, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGehee, K., McPhee, K., McPhee, N., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Milne, V., Morrow, Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, T. M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Poliara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., Young, G., Zainoun, J., Zimmer, A., and Zody, M.				
COMMENT	Direct Submission				
TITLE	Submitted (20-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA				
JOURNAL	On Jun 28, 2000 this sequence version replaced gi:8516129.				
COMMENT	All repeats were identified using RepeatMasker:				

Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L9800
 Center clone name: 112_B_11
 ----- Summary Statistics
 Sequencing vector: M11; M7815; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 1.55611 bases at least Q40
 Consensus quality: 1.56805 bases at least Q30
 Consensus quality: 1.56332 bases at least Q20
 Insert size: 168000; agarose-fp
 Insert size: 159274; sum-of-contigs
 Quality coverage: 4.5 in Q20 bases; agarose-fp
 Quality coverage: 4.7 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 15 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 1886: contig of 1886 bp in length
 * 1887 1986: gap of 100 bp
 * 1987 4579: contig of 2593 bp in length
 * 4580 4679: gap of 100 bp
 * 4680 8193: contig of 3514 bp in length
 * 8194 8293: gap of 100 bp
 * 8294 12006: contig of 3713 bp in length
 * 12007 12163: gap of 100 bp
 * 12107 16432: contig of 4326 bp in length
 * 16433 16532: gap of 100 bp
 * 16533 21956: contig of 5424 bp in length
 * 21957 22036: gap of 100 bp
 * 22057 28704: contig of 6648 bp in length
 * 28705 28804: gap of 100 bp
 * 28805 36083: contig of 7279 bp in length
 * 36084 36133: gap of 100 bp
 * 36184 47720: contig of 11537 bp in length
 * 47721 47820: gap of 100 bp
 * 47821 58804: contig of 10984 bp in length
 * 58805 58904: gap of 100 bp
 * 58905 73884: contig of 14980 bp in length
 * 73885 73994: gap of 100 bp
 * 73985 88999: contig of 15005 bp in length
 * 88990 89099: gap of 100 bp
 * 89090 104855: contig of 15766 bp in length
 * 104855 104955: gap of 100 bp
 * 104956 125506: contig of 20551 bp in length
 * 125507 125606: gap of 100 bp
 * 125607 160674: contig of 35068 bp in length.

FEATURES
 source
 misc_feature
 misc_feature
 misc_feature

Location/Qualifiers
 1. 1160674
 /organism="Homo sapiens"
 /db_xref="Taxon:9606"
 /chromosome="2"
 /map="2"
 /clone="RP11-112B11"
 1. .1886
 /note="assembly_fragment"
 1987. 4579
 /note="assembly_fragment"
 4680. .8193
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Search completed: November 26, 2001, 10:03:06
Job time: 2816 sec